

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/061,417OICE #3
DATE: 04/23/98
TIME: 15:39:23
06/18/98

INPUT SET: S25265.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Olson, Eric N.
6 Grant, Stephen R.
7 Molkentin, Jeffrey D.
8
9 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THERAPEUTIC
10 INTERVENTION IN CARDIAC HYPERTROPHY
11
12 (iii) NUMBER OF SEQUENCES: 9
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Arnold, White & Durkee
16 (B) STREET: P.O. Box 4433
17 (C) CITY: Houston
18 (D) STATE: Texas
19 (E) COUNTRY: USA
20 (F) ZIP: 77210
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
--> 29 (A) APPLICATION NUMBER: US Unknown
30 (B) FILING DATE:
--> 31 (C) CLASSIFICATION: Unknown
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: McMillian, Nabeela R.
35 (B) REGISTRATION NUMBER: P-43,363
36 (C) REFERENCE/DOCKET NUMBER: UTSD:548
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 512/418-3000
40 (B) TELEFAX: 512/474-7577
41
42
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 23 base pairs

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47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: linear
50
51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
52
53 CTATCCTTTT GTTTTCCATC CTG 23
54
55
56 (2) INFORMATION FOR SEQ ID NO:2:
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58 (i) SEQUENCE CHARACTERISTICS:
59 (A) LENGTH: 23 base pairs
60 (B) TYPE: nucleic acid
61 (C) STRANDEDNESS: single
62 (D) TOPOLOGY: linear
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
65
66 TCCCTGCCTT TTCCAGCAAC GGT 23
67
68
69 (2) INFORMATION FOR SEQ ID NO:3:
70
71 (i) SEQUENCE CHARACTERISTICS:
72 (A) LENGTH: 23 base pairs
73 (B) TYPE: nucleic acid
74 (C) STRANDEDNESS: single
75 (D) TOPOLOGY: linear
76
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
78
79 GCTCCAGGAT AAAAGGCCAC GGT 23
80
81
82 (2) INFORMATION FOR SEQ ID NO:4:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 23 base pairs
86 (B) TYPE: nucleic acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
91
92 TACATTGGAA AATTTTATTA CAC 23
93
94
95 (2) INFORMATION FOR SEQ ID NO:5:
96
97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 10 base pairs
99 (B) TYPE: nucleic acid

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100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
104
105 TGGAAAACAA 10
106
107
108 (2) INFORMATION FOR SEQ ID NO:6:
109
110 (i) SEQUENCE CHARACTERISTICS:
111 (A) LENGTH: 10 base pairs
112 (B) TYPE: nucleic acid
113 (C) STRANDEDNESS: single
114 (D) TOPOLOGY: linear
115
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
117
118 TGGAAAAGGC 10
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120
121 (2) INFORMATION FOR SEQ ID NO:7:
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123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 10 base pairs
125 (B) TYPE: nucleic acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
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129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
130
131 AGGATAAAAG 10
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133
134 (2) INFORMATION FOR SEQ ID NO:8:
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136 (i) SEQUENCE CHARACTERISTICS:
137 (A) LENGTH: 902 amino acids
138 (B) TYPE: amino acid
139 (C) STRANDEDNESS:
140 (D) TOPOLOGY: linear
141
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
143
144 Met Gly Ala Ala Ser Cys Glu Asp Glu Glu Leu Glu Phe Leu Leu Val
145 1 5 10 15
146
147 Phe Gly Glu Glu Leu Glu Ala Pro Pro Leu Gly Ala Gly Gly Leu Gly
148 20 25 30
149
150 Glu Glu Leu Asp Ser Glu Asp Ala Pro Pro Cys Cys Arg Leu Ala Leu
151 35 40 45
152

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153	Gly	Glu	Pro	Pro	Pro	Tyr	Gly	Ala	Ala	Pro	Ile	Gly	Ile	Pro	Arg	Pro
154		50					55					60				
155																
156	Pro	Pro	Pro	Arg	Pro	Gly	Met	His	Ser	Pro	Pro	Pro	Arg	Pro	Ala	Pro
157	65					70					75					80
158																
159	Ser	Pro	Gly	Thr	Trp	Glu	Ser	Gln	Pro	Ala	Arg	Ser	Val	Arg	Leu	Gly
160					85					90					95	
161																
162	Gly	Pro	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Gly	Arg	Val	Leu	Glu
163					100				105					110		
164																
165	Cys	Pro	Ser	Ile	Arg	Ile	Thr	Ser	Ile	Ser	Pro	Thr	Pro	Glu	Pro	Pro
166			115					120					125			
167																
168	Ala	Ala	Leu	Glu	Asp	Asn	Pro	Asp	Ala	Trp	Gly	Asp	Gly	Ser	Pro	Arg
169		130					135					140				
170																
171	Asp	Tyr	Pro	Pro	Pro	Glu	Gly	Phe	Gly	Gly	Tyr	Arg	Glu	Ala	Gly	Ala
172	145					150					155					160
173																
174	Gln	Gly	Gly	Gly	Ala	Phe	Phe	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Ser	Leu
175					165					170						175
176																
177	Ser	Ser	Trp	Ser	Phe	Phe	Ser	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Leu	Tyr
178				180					185					190		
179																
180	Ala	Ala	Cys	Asp	Glu	Val	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Ala	Ser	Arg
181			195					200					205			
182																
183	Phe	Gly	Leu	Gly	Ser	Pro	Leu	Pro	Ser	Pro	Arg	Ala	Ser	Pro	Arg	Pro
184		210					215					220				
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186	Trp	Thr	Pro	Glu	Asp	Pro	Trp	Ser	Leu	Tyr	Gly	Pro	Ser	Pro	Gly	Gly
187	225					230					235					240
188																
189	Arg	Gly	Pro	Glu	Asp	Ser	Trp	Leu	Leu	Leu	Ser	Ala	Pro	Gly	Pro	Thr
190					245					250					255	
191																
192	Pro	Ala	Ser	Pro	Arg	Pro	Ala	Ser	Pro	Cys	Gly	Leu	Arg	Arg	Tyr	Ser
193				260					265					270		
194																
195	Ser	Ser	Gly	Thr	Pro	Ser	Ser	Ala	Ser	Pro	Ala	Leu	Ser	Arg	Arg	Gly
196			275					280					285			
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198	Ser	Leu	Gly	Glu	Glu	Gly	Ser	Glu	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro
199		290					295					300				
200																
201	Leu	Ala	Arg	Asp	Pro	Gly	Ser	Pro	Gly	Pro	Phe	Asp	Tyr	Val	Gly	Ala
202	305					310					315					320
203																
204	Pro	Pro	Ala	Glu	Ser	Ile	Pro	Gln	Leu	Thr	Arg	Arg	Thr	Ser	Ser	Glu
205					325					330					335	

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206																			
207	Gln	Ala	Val	Ala	Leu	Pro	Arg	Ser	Glu	Glu	Pro	Ala	Ser	Cys	Asn	Gly			
208				340					345					350					
209																			
210	Leu	Leu	Pro	Leu	Gly	Ala	Glu	Glu	Ser	Val	Ala	Pro	Pro	Gly	Gly	Ser			
211			355					360					365						
212																			
213	Arg	Lys	Glu	Val	Ala	Gly	Met	Asp	Tyr	Leu	Ala	Val	Pro	Ser	Pro	Leu			
214		370					375					380							
215																			
216	Ala	Trp	Ser	Leu	Ala	Arg	Ile	Gly	Gly	His	Ser	Pro	Ile	Phe	Arg	Thr			
217	385					390				395						400			
218																			
219	Ser	Ala	Leu	Pro	Pro	Leu	Asp	Trp	Pro	Leu	Pro	Ser	Gln	Tyr	Glu	Gln			
220				405						410					415				
221																			
222	Leu	Glu	Leu	Arg	Ile	Glu	Val	Gln	Pro	Arg	Ala	His	His	Arg	Ala	His			
223				420					425					430					
224																			
225	Tyr	Glu	Thr	Glu	Gly	Ser	Arg	Gly	Ala	Val	Leu	Ala	Ala	Pro	Gly	Gly			
226			435					440					445						
227																			
228	His	Pro	Val	Val	Leu	Leu	Leu	Gly	Tyr	Ser	Glu	Leu	Pro	Leu	Thr	Leu			
229		450					455					460							
230																			
231	Gln	Met	Phe	Ile	Gly	Thr	Ala	Asp	Glu	Arg	Asn	Leu	Arg	Pro	His	Ala			
232	465					470					475					480			
233																			
234	Phe	Tyr	Gln	Val	His	Arg	Ile	Thr	Gly	Leu	Met	Val	Ala	Thr	Ala	Ser			
235					485					490					495				
236																			
237	Tyr	Glu	Ala	Val	Val	Ser	Gly	Thr	Leu	Val	Leu	Glu	Met	Thr	Leu	Leu			
238				500					505					510					
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240	Pro	Glu	Asn	Asn	Met	Ala	Ala	Asn	Ile	Asp	Cys	Ala	Gly	Ile	Leu	Leu			
241			515					520					525						
242																			
243	Leu	Arg	Asn	Ser	Asp	Ile	Glu	Leu	Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly			
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246	Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu	Val	Phe	Arg	Val	His	Val	Pro	Gln			
247	545					550					555					560			
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249	Gly	Gly	Gly	Leu	Val	Val	Ser	Val	Gln	Ala	Ala	Ser	Val	Pro	Ile	Glu			
250				565					570					575					
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252	Cys	Ser	Gln	Arg	Ser	Ala	Gln	Glu	Leu	Pro	Gln	Val	Glu	Ala	Tyr	Ser			
253				580					585					590					
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255	Pro	Ser	Ala	Cys	Ser	Val	Arg	Gly	Gly	Glu	Glu	Leu	Val	Leu	Thr	Gly			
256			595					600					605						
257																			
258	Ser	Asn	Phe	Leu	Pro	Asp	Ser	Leu	Val	Val	Phe	Ile	Glu	Arg	Gly	Pro			

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/061,417*

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Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: US Unknown
31	Wrong Classification	(C) CLASSIFICATION: Unknown